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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/667,188	09/21/2000	Scott E. Andersen	38-21(51464)B	8378

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EXAMINER	
BAUSCH, SARAE L	

ART UNIT	PAPER NUMBER
1634	

DATE MAILED: 09/07/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	09/667,188	ANDERSEN ET AL.	
	Examiner	Art Unit	
	Sarae Bausch	1634	

-- *The MAILING DATE of this communication appears on the cover sheet with the correspondence address* --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *07/02/2004*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,2 and 11-15* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-2,11-15* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *Detailed Action*.

DETAILED ACTION

The examiner reviewing your application at the PTO has changed. To aid in correlating any papers for this application, all further correspondence regarding this application should be directed to examiner Sarae Bausch.

1. Currently, claims 1-2 and 11-15 are pending in the instant application. Claims 3-10 have been canceled. All the amendments and arguments have been thoroughly reviewed but were found insufficient to place the instantly examined claims in condition for allowance. The following rejections are either newly presented, as necessitated by amendment, or are reiterated from the previous office action. They represent the complete being presently applied to the instantly examined claims. Response to arguments follow. This action is FINAL.

2. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

3. The objections made to the specification regarding an embedded hyperlink is withdrawn in view of the amendment to the specification.

4. The rejections made to claims 1 and 2 under 35 USC 112, second paragraph, on page 19 of the previous office action is withdrawn in view of the amendments to claims 1 and 2.

Maintained Rejections

Claim Rejections - 35 USC § 101

5. The rejection of claims 1, 2, 11-15 made under 35 U.S.C. 101, in the previous office action is maintained and incorporated herein, as are the responses to arguments (see pages 2-13

of the previous office action mailed 02/02/2004). However, it is noted that the sentence at page 4, which begins at line 8: "Note, because the claimed invention is not supported by a specific and substantial asserted utility for the reasons set forth above, credibility has not been assessed." is withdrawn because it is clear from the examiners response to arguments that in fact, credibility of the asserted uses has been assessed by the previous office action (see office action, page 12, section titled "Credible Utility") which states "while the disclosed utilities of the present invention are credible, they are not specific or substantial.".

Response to Arguments

6. The response traverses the rejection under 35 U.S.C. 101. In the 2nd- 3rd paragraphs of page 6; the response traverses that the nucleic acid can be utilized for identifying the presence or absence of a polymorphism, isolating specific promoter sequences, and to obtain nucleic acid homologs. The response cited Raytheon Co. v. Roper Corp. (Fed. Cir. 1983) as support that since "the properly claimed invention meets at least one stated objective, utility under section 101 is clearly shown." This argument has been thoroughly reviewed but was not found persuasive as these uses stated in the specification are neither specific nor substantial for the reason already made of record in the previous office actions. In addition, the analogy is made that the "disclosed utilities in this case, including the detection of polymorphisms, are directly analogous to the utilities of a microscope". This argument was thoroughly reviewed but not found persuasive because the nucleic acid of the present invention is not analogous to a microscope. A microscope has a specific and substantial utility of magnifying images to allow the visualization of items too small to be seen by the unaided eye. This utility is specific for a microscope and is based on the physical structure of the lenses and mirrors present within the

microscope. Applicants are effectively traversing that a nucleic acid and microscope are analogous because they can be used as a research tool. However, the claimed nucleic acid can only be used to detect sequences that themselves have no specific and substantial utility. This is analogous to the disclosure of a microscope containing a slide which contains an unknown smear of matter and providing claims to the unknown smear of matter. In regards to SEQ ID NO: 1, it is a fragment of a larger sequence that has no described function that would allow one to identify a specific plant protein product as recited by the claims. However neither the sequence of SEQ ID NO 1, nor the protein it encodes, are supported by a specific or substantial utility or a well established utility. With respect to the detection of polymorphisms being a specific and substantial utility, the argument is not convincing because the detection of a polymorphisms is not useful until the polymorphisms is associated with a disease or other specific characteristic of interest to the public.

On page 7, the response traverses that there is "no requirement for exclusive utility" with respect to other molecules also being used for the same purpose as the polynucleotide; "[s]uch an argument would imply that a new golf club has no legal utility because other golf clubs can be used for the same purpose, *i.e.* hitting golf balls." The argument is not persuasive because in the golf club case - a golf club has a specific and substantial utility and therefore an improved golf club for instance, would as well. This utility is directly dependent upon the structure of the golf club and the materials of which it is composed. In the instant case, no specific or substantial utility has been established for the claimed nucleic acid. A golf club is not structurally or functionally analogous to the nucleic acid of the present invention. Thus to be able to hit a golf ball in an effective and controlled manner because of the structure and composition of the club is

a real world context of use, and is immediately apparent with no further experimentation needed to determine its use, whereas the unique combination of the nucleotides within a nucleic acid molecule determines its specific function or activities; however in the instant case, further experimentation is required to determine its function or activities. The asserted utilities for the present invention do not take advantage of the particular combination of nucleic acids in the present invention but rather rely on properties common to all nucleic acids. The utility is therefore considered non-specific.

On page 8, paragraph 1, the response traverses that the claimed nucleic acid molecules encompass many utilities, some of which may be common to a broad class of molecules. The response asserts that while all nucleic acids can be generally used to isolate related sequences, the claimed nucleic acid will identify a unique subset of related sequence. This argument has been thoroughly reviewed but was not found persuasive because the specification has not provided a specific or substantial utility for this "unique subset of related sequences". The reason that such a utility is neither specific nor substantial in the instant case is because all nucleic acids can be used to identify a "unique set of related sequences". As no apparent specific, substantial, or real world utility has been provided for such "unique set of related sequences", no specific, substantial, or real world utility is provided for the claimed SEQ ID NO just because it can be used to identify a unique set of related sequences. As this applies to the golf club analogy, it is noted that the golf club is being used to hit a golf ball, which also has a specific substantial, and readily apparent real world use.

On page 8, paragraph 2, the response traverses that a person of ordinary skill in the art would recognize that the claimed nucleic acid molecules have utility, given the teachings of the

specification at pages 33-34 and 86. This argument as well as the specification have been thoroughly reviewed but were not found to be persuasive because the specification provides no specific, or substantial utility for the claimed nucleic acid, nor does a real world utility exist for the claimed nucleic acid at the time the application was filed. The nucleic acid sequence of SEQ ID NO: 1 appears to be a fragment of a larger protein since it was isolated from a *Triticum aestivum* cDNA library. However the specification has provided no teachings as to a function for a protein encoded by isolated SEQ ID NO: 1 nor any of the remaining 8134 sequences also isolated from the cDNA library and provides no description of the remainder of the coding sequence of which SEQ ID NO: 1 is a fragment. The specification teaches no function or activity for the protein that SEQ ID NO: 1 might encode, nor teaches which "important genes" associated with plant growth, quality, and yield would be isolated by the claimed Seq ID NO: 1, or what "important developmental, metabolic, and catabolic pathways" Seq ID NO:1 may be a link to. Plant nucleic acids, in general, could be used to "isolate agronomically important genes associated with plant growth, quality, and yield" and could serve as "links in important developmental, metabolic and catabolic pathways." However, the specification provides no specific, or substantial utility that takes advantage of the particular combination of nucleotides in the presently claimed nucleic acid molecule.

With regard to applicants' comments regarding credible utility (p.9 to p. 10), such arguments are considered moot because the assertion that credibility has not been assessed is withdrawn (see section 5 above). It is clear from the previous office action that credibility was in fact assessed (see page 12 of previous office action, section titled "Credible Utility") and not found to be lacking. Please note, the examiner is not challenging the credibility of the instant

invention. However, the fact that the asserted utilities of the present invention are credible does not in any way affect the fact that the asserted utilities are non-specific and not substantial. The claimed invention lacks a specific and substantial asserted utility for the reasons made of record above and in previous office actions. The rejection of claims 1, 2, and 11-15 is therefore maintained.

Claim Rejections - 35 USC § 112

Enablement

7. The rejection of claims 1, 2, 11-15 made under 35 U.S.C. 112, 1st paragraph (enablement), in the previous office action is maintained and incorporated herein, as are the responses to arguments (see pages 12-13 of the previous office action mailed 02/02/2004).

Response to Arguments

8. On page 10, section III, the response traverses that the enablement requirements of the claim have been met for reasons that the rejections under 35 U.S.C. 101 have been overcome. This argument has been thoroughly reviewed but was not found to be persuasive because of the reasons as set forth in section 6 above. The claimed invention is not supported by either a specific or substantial asserted utility. As such, one skilled in the art clearly would not know how to use the claimed invention. For these reasons, and the reasons made of record in the previous office actions, the rejection is maintained.

Written Description

9. The rejection of claims 1, 2, 11-15 made under 35 U.S.C. 112, 1st paragraph (written description), in the previous office action is maintained and incorporated herein, as are the responses to arguments (see pages 13-19 of the previous office action mailed 02/02/2004).

Response to Arguments

10. On page 10-12, section IV, the response traverses that a person of ordinary skill in the art would, after reading the present specification, understand that Applicants had possession of SEQ ID NO:1; and the complement and variations thereof. This argument has been thoroughly reviewed but was not found to be persuasive because the specification only describes a nucleic acid that is not a full-length open reading frame, but an EST, which has the sequence of SEQ ID NO: 1. Claims 1, 2 and 11-12 encompass variants and homologs, as well as full-length open reading frames of undisclosed proteins from any source (claims 1, 2, 11). Further, claims 13-15 encompass variants, mutants and homologs from any source. The claims therefore encompass a very large variable genus. Beyond providing the sequence data for SEQ ID NO: 1, however, the specification provides no teaching or guidance which correlates the sequence of SEQ ID NO: 1 to its function, which amino acids in the protein encoded by SEQ ID NO: 1 are critical to its function, or how to modify SEQ ID NO: 1 to obtain any specific homolog, mutant, or variant. It is not clear which positions with SEQ ID NO: 1 can be substituted or altered without resulting in a loss of the function of SEQ ID NO: 1. Therefore, the skilled artisan would be unable to determine whether or not a DNA molecule is functionally equivalent to SEQ ID NO: 1. The claims provide for a large genus of nucleic acids that include undisclosed genes, partial genomic sequences, mutants, variants, and homologs of SEQ ID NO: 1, however the single disclosed

structural feature of SEQ ID NO: 1 does not provide for a substantial portion of the claimed genus.

The response asserts that the specification has disclosed "SEQ ID NO: 1 and the complements and variations thereof" (paragraph bridging pp. 12-13), pointing to the description of vectors, the libraries from which the nucleotides were purified, contemplation of labels or markers for facilitated detection, site directed mutagenesis, *etc.* that encompass describing the possible variations of SEQ ID NO: 1, that are read on by the claims. This argument has been thoroughly reviewed but is not found to be persuasive because the specification does not reflect possession of mutants, variants, or homologs of SEQ ID NO: 1 from any source by merely disclosing the sequence of SEQ ID NO: 1 and general descriptions on how to alter it. For example, placing SEQ ID NO: 1 in a vector does not reflect possession of mutants or variants of SEQ ID NO: 1. The various sections of the specification cited in the response describe how to find sequences, which are encompassed by the scope of the claims. Such is not the same as describing what these sequences, full genes, genomic sequences, mutants, variants, and homologs actually are. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it. The nucleic acid itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (CAFC 1993) and *Amgen Inc. V. Chugai Pharmaceutical Co. Ltd.,* 18 USPQ2d 1016.

The response asserts that "the respective common structural feature (the nucleotide sequence of SEQ ID NO: 1 and its complement) is shared by every nucleic acid molecule in this claimed genera" (1st paragraph, p. 14) thus those sequences of percent sequence identity are taught by the specification. This response was thoroughly reviewed and was not found

persuasive because the disclosure of SEQ ID NO:1 does not provide a written description of the genes or genomic sequences encompassed by a claim reciting "nucleic acid comprising the sequence of SEQ ID NO: 1 or the complement thereof". It is additionally noted that the claims till recite "a nucleic acid sequence" or "a complement" which provides that only a few nucleotides from SEQ ID NO: 1 be present in the claimed molecule. The previous office action on page 14 clearly shows that such recitation encompasses an enormous genus, of which the sequence of SEQ ID NO: 1 is not representative.

On page 14, paragraph 2, the response asserts that the nucleic acid molecules falling within the scope of the present claims are readily identifiable, they share % sequence identity. This argument was thoroughly reviewed but was not found persuasive because while one of skill in the art could argue that the claimed genus of polynucleotides is adequately described since one can isolate these polynucleotides by sequence comparison using the polypeptide/polynucleotide structures disclosed in the instant application or the prior art, the state of the art teaches that sequence comparison alone cannot be used reliably to determine a protein's function and that small amino acid changes can drastically change the function of a polypeptide. The specification teaches SEQ ID NO: 1, a 332 bp sequence, yet fails to describe a reading frame that would encode a protein or protein fragment as desired by the claim. Assuming arguendo the reading frame was known, the 1%-5% difference in sequence not disclosed can destroy the protein or protein fragment to be encoded. Any percent difference can greatly alter structure and/or function of the resulting peptide. Bork [Genome Research, 10: 398-400 (2000)] teaches protein function is context dependent, and both molecular and cellular aspects must be considered (page 398). Van de Loo et al. [PNAS 92; 6743-6747 (1995)] teaches that polypeptides of

approximately 67% homology to a desaturase from *Arabidopsis* were found to be hydroxylases once tested for activity. Seffernick et al. [J. Baceriol. 183 (8); 2405-2410 (2001)] teaches that two naturally occurring Pseudomonas enzymes having 98% amino acid sequence identity catalyze two different reactions: deamination and dehalogenation, therefore having different function. Broun et al. [Science 282: 1315-1317 (1998)] teaches that as few as four amino acid substitutions can convert an oleate 12-desaturase into a hydroxylase and as few as six amino acid substitutions can transform a hydroxylase to a desaturases. The genus of polynucleotides comprised by the claim is a large variable genus, which can potentially encode proteins of diverse functions. The specification only discloses a single species of the genus, i.e. the polynucleotide of SEQ ID NO: 1, which is insufficient to put one of skill in the art in possession of all attributes and features of all species within the genus. Thus one skilled in the art cannot reasonably conclude that applicant had possession of the claimed invention at the time the instant application was filed. For these reasons, and the reasons made of record in the previous office actions, the rejection is maintained.

Claim Rejections - 35 USC § 102

11. Claims 1, 2 and 11-15 are rejected under 35 U.S.C. 102(a) as being anticipated by the GenBank accession number BE428765 (26-July-2000).

The GenBank accession number BE428765 is a mRNA from the wheat plant Triticum turgidum and comprises a nucleic acid sequence of SEQ ID NO: 1 (for example, nucleic acid positions 46-251 of SEQ ID NO: 1). The aligned sequence segment of positions 98-303 is 100% identical to SEQ ID NO: 1. A nucleic acid molecule or a fragment of nucleic acid positions 46-

251 of SEQ ID NO: 1 would be a complete complement to the accession number positions 98-303, therefore the instant accession number anticipates the claimed nucleic acid. In addition, please note that even a minimum of a two base pair sequence anticipates claim 2 due to the claim language "fragment". With respect to claim 15, the recitation of "comprises a region having a single nucleotide polymorphism [SNP]" does not structurally limit claim 13. Any sequence can potentially comprise a SNP and depends on what one is comparing it to. Therefore the GenBank accession number BE42765 anticipates claims 1, 2 and 11-15 as a nucleic acid molecule comprising of a nucleic acid sequence of SEQ ID NO: 1.

12. Claims 1, 2 and 11-15 are rejected under 35 U.S.C. 102(b) as being anticipated by the GenBank accession number AI861202 (19-July-1999).

The GenBank accession number AI861202 is a mRNA from the plant Zea mays and comprises a nucleic acid sequence of SEQ ID NO: 1 (for example, nucleic acid positions 314-332 of SEQ ID NO: 1. The aligned sequence segment of positions 169-187 is 100% identical to SEQ ID NO: 1. A nucleic acid molecule or a fragment of nucleic acid positions 314-332 of SEQ ID NO: 1 would be a complete complement to the accession number nucleotide positions 169-187, therefore the instant accession number anticipates the claimed nucleic acid. In addition, please note that even a minimum of a two base pair sequence anticipates claim 2 due to the claim language "fragment". With respects to claim 15, the recitation of "comprises a region having a single nucleotide polymorphism [SNP]" does not structurally limit claim 13. Any sequence can potentially comprise a SNP and depends on what one is comparing it to. Therefore the GenBank

accession number AI861202 anticipates claims 1, 2 and 11-15 as a nucleic acid molecule comprising or consisting of **a** nucleic acid sequence of SEQ ID NO: 1.

Response to Arguments

13. The response asserts that claims 1,2, and 11-15 have been amended to overcome the rejections under 35 U.S.C. 102 by reciting "complete complement thereof" and deleting the recitation of "fragment thereof". This argument has been thoroughly reviewed but was not found persuasive. The amendment does not overcome the rejection set forth by GenBank Accesion Nos BE428765 and A1861202 because each teach a nucleotide comprising "a" sequence and "a" complete complement of SEQ ID NO:1. It is acknowledged that the GenBank Accesion Nos BE428765 and A1861202 do not teach "the" sequence of SEQ ID NO:1 nor "the" complete complement of SEQ ID NO:1; however, the claims recite "a" sequence and "a" complete complement of SEQ ID NO:1, which encompass the sequences in GenBank Accesion Nos BE428765 and A1861202. The amendment does not overcome the rejection as comprising " complete complement" can be broadly interpreted to mean any sequence that comprises a region, which is "a" complete complement to "a" sequence of SEQ ID NO:1. Further, it is noted that claim 2 continues to recite "fragment thereof". Therefore, arguments that such terminology has been deleted is additionally not persuasive with regard to claim 2. For these reasons, and the reasons made of record in the previous office actions, the rejection is maintained.

Claim Rejections - 35 USC § 102

14. Claims 1, 2 and 11-15 are rejected under 35 U.S.C. 102(b) as being anticipated by products O3628 and O4378 of the 1993 SIGMA Chemical Catalog.

In The 1993 Sigma Chemical Catalog product O3628 is a 7-mer oligonucleotide of poly dT nucleotides and product O4378 is a 4-mer oligonucleotide of poly dA nucleotides, both of which are 100% identical to a nucleic acid sequence of SEQ ID NO: 1. It is noted that these oligonucleotides are at least about 95%-100% (and 99%-100%) identical to poly T segments or their complementary respective poly A segments of the instantly claimed nucleic acids. They thus anticipate instant claims 1 and 11-14 via segments therein which are poly T segments or poly A segments present in the SEQ ID NO: 1 (nucleic acid positions 7-15 and 189-193 respectively). In addition, please note that even a minimum of a two base pair sequence anticipates claim 2 due to the claim language "fragment". With respects to claim 15, the recitation of "comprises a region having a single nucleotide polymorphism [SNP]" does not structurally limit claim 13. Any sequence can potentially comprise a SNP and depends on what one is comparing it to. Therefore the O3628 and O4378 products anticipate claims 1, 2 and 11-15 as a nucleic acid molecule comprising or consisting of a nucleic acid sequence of SEQ ID NO: 1.

Response to Arguments

15. The response asserts that claims 1,2, and 11-15 have been amended to overcome the rejections under 35 U.S.C. 102 by reciting "complete complement thereof" and deleting the recitation of "fragment thereof". This argument has been thoroughly reviewed but was not found persuasive. The amendment does not overcome the rejection set forth by products O3628 and O4378 from the 1993 SIGMA Chemical Catalog, as O3628 and O4378 because each teach a nucleic acid comprising "a" sequence and "a" complete complement of SEQ ID NO:1. It is acknowledged that the products O3628 and O4378 do not teach "the" sequence of SEQ ID NO: 1

nor "the" complement of SEQ ID NO:1, however the claims recite "a" sequence and complete complement of SEQ ID NO:1, which encompass the sequences in products O3628 and O4378. The amendment does not overcome the rejection as comprising "complete complement" can be broadly interpreted to mean sequences that comprises a region which is "a" complete complement to "a" sequence of SEQ ID NO: 1. Further it is noted that claim 2 continues to recite "fragment thereof". Therefore, arguments that such terminology has been deleted is additionally not persuasive with regard to claim 2.

Conclusion

16. **THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Sarae Bausch whose telephone number is (571) 272-2912. The examiner can normally be reached on M-F 9am-5pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on (571) 272-0782. The fax phone number for the organization where this application or proceeding is assigned is (703) 872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at (866) 217-9197 (toll-free).

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

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Jehanne Sitton
JEHANNE SITTON
PRIMARY EXAMINER
9/2/04

Sarae Bausch, PhD.
Examiner
Art Unit 1634